

SCORE Search Results Details for Application 10552515 and Search Result 20080624_083152_us-10-552-515-1.rpr.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10552515 and Search Result 20080624_083152_us-10-552-515-1.rpr.

[Go Back to previous page](#)

GenCore version 6.2.1

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OM protein - protein search, using sw model

Run on: June 24, 2008, 08:36:37 ; Search time 36 Seconds
(without alignments)
2493.618 Million cell updates/sec

Title: US-10-552-515-1
Perfect score: 4950
Sequence: 1 MRMAATAWAGLQGPPLPTLC.....SELSSHWTPTFVPKASQLQQ 933

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	734	14.8	1049	2	T22762	hypothetical prote
2	288.5	5.8	572	2	F96755	hypothetical prote
3	181.5	3.7	946	2	S48255	probable membrane
4	117	2.4	548	2	I48693	natural resistance
5	115.5	2.3	3010	1	GNWVTC	genome polyprotein
6	110.5	2.2	680	2	T35404	probable squalene-
7	110.5	2.2	873	2	S46584	probable membrane
8	110	2.2	792	2	T00487	probable potassium

9	108	2.2	3010	1	A45573	genome polyprotein
10	106.5	2.2	519	2	T11129	cytochrome-c oxida
11	106	2.1	438	2	B86088	probable citrate p
12	106	2.1	438	2	E91240	probable membrane
13	105	2.1	621	2	JC1346	dopamine beta-mono
14	104	2.1	646	2	H82555	c-type cytochrome
15	103.5	2.1	478	2	JQ2034	RNA-directed RNA p
16	102	2.1	302	2	C83993	hypothetical prote
17	101.5	2.1	395	2	D81040	cytochrome c-type
18	101.5	2.1	395	2	B81986	probable membrane
19	101	2.0	466	2	A95355	probable inner-mem
20	100.5	2.0	585	2	S74673	pleD protein - Syn
21	100	2.0	515	2	D71390	cytochrome-c oxida
22	100	2.0	3010	1	GNWVCJ	genome polyprotein
23	99.5	2.0	737	2	AG2156	hypothetical prote
24	98.5	2.0	413	2	AF0393	NADH2 dehydrogenas
25	98.5	2.0	1353	2	T26301	hypothetical prote
26	98.5	2.0	1755	2	S69845	TyB protein - yeas
27	98	2.0	348	2	T12280	NADH2 dehydrogenas
28	98	2.0	1265	2	T51314	probable CO-induce
29	97.5	2.0	348	2	T12291	NADH2 dehydrogenas
30	97.5	2.0	348	2	T12290	NADH2 dehydrogenas
31	97.5	2.0	460	2	A84154	amino acid transpo
32	97.5	2.0	906	2	G83156	probable transcrip
33	96.5	1.9	348	2	T12281	NADH2 dehydrogenas
34	96.5	1.9	417	2	C81084	probable integral
35	96.5	1.9	491	2	B70414	NADH2 dehydrogenas
36	96.5	1.9	1755	2	S69969	TyB protein - yeas
37	96	1.9	419	1	SYPIJD	naringenin-chalcon
38	96	1.9	428	2	T48284	hypothetical prote
39	96	1.9	865	2	T40288	hypothetical prote
40	95.5	1.9	572	2	T48601	hypothetical prote
41	95.5	1.9	758	2	D71072	hypothetical prote
42	95.5	1.9	1755	2	S50663	TyB protein - yeas
43	95	1.9	429	2	AG3150	hypothetical prote
44	95	1.9	473	2	AC0479	glycerol-3-phospha
45	95	1.9	631	2	B98137	hypothetical 46.1K

ALIGNMENTS

RESULT 1
T22762
hypothetical protein F56A8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22762
R;McMurray, A.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19612
A;Accession: T22762
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1049 <WIL>
A;Cross-references: UNIPROT:O45572; UNIPARC:UPI000007F44C; EMBL:Z83230; PIDN:CAB05741.1; GSPDB:GN00021; CESP:F56A8.1
A;Experimental source: clone F56A8
C;Genetics:
A;Gene: CESP:F56A8.1
A;Map position: 3
A;Introns: 86/3; 146/3; 208/3; 245/2; 295/2; 325/2; 397/3; 532/3; 582/2; 612/3; 654/1; 677/1; 707/3; 734/3; 786/2; 812/2; 870/1; 902/3; 942/3; 1011/2

C;Superfamily: Caenorhabditis elegans hypothetical protein F56A8.1

Query Match	14.8%;	Score 734;	DB 2;	Length 1049;
Best Local Similarity	27.0%;	Pred. No. 9.2e-54;		
Matches	248;	Conservative 137;	Mismatches 309;	Indels 224; Gaps 32;
Qy	96	AAACRAGSPAKP-RIA-DFVLVWEEDLKLDQRQDSAAARDTDMHRTWRETFLDNLRAAGL	153	
Db	3	AATTEVDVYPYFFRISIDFVLV-----HNAAESRS--KGKYREFFEKAVQKEGL	49	
Qy	154	CVDQDDVQDGNTTVHYALLSASWAVLCYYAEDLRLLKPLQELPNQASNWSAGLLAWLGIP	213	
Db	50	IIRHQ--QSGQT--HFTLISTPFHRLTREAEMSQMFPLKDKQVKP-----GLP	94	
Qy	214	NVLLEV---VPDVPPEYSCRFRVFNKLPRFLGSDNQDTFFTTSTKRHQILFEILAKTPYG	269	
Db	95	SCCIPLSQIFVTDITVRFINAPFFQRKHGSLFLNYHDEKSFSTTSQRGYLYTQILTKIDIS	154	
Qy	270	HEKK-----NLLGIHQLLAEGVLSAAFLH-----	294	
Db	155	KDLKGERLGESQDEPTDPSTSSITSDEQLRRKGLSWLLMSDVYEEAFVLHAPSKEEYFK	214	
Qy	295	---DGPFKTPPEGPQAPRLNQOVLFQHWARWGKWKYQPLDHRVRYFGEKVALYFAWL	351	
Db	215	AMQNGSVKAYNEFISEIELDPRRSLSLNWER---WYKFOPLNKIRDYFGEQIAYFAWQ	271	
Qy	352	FYTGWLLPAAVVGLTVFLVGCFLVFS DIP-----TQEL-CGSKDS----FE	392	
Db	272	TFLTLLWPAVIFGLVVFYIGFIDISSAPLDWNHCKVVNFQGTENVACGMNRNGVTLFFS	331	
Qy	393	MCPLCLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRW	452	
Db	332	MVTQ-----WFMSS-----FDTKMAFFAVFMSIWGSVFVQIWRKNSVLSYQW	375	
Qy	453	DCSDYEDTEERPRQFAASAPMTAPNPITGEDEPYFFPERSARRMLAGSVIVVMVAVVV	512	
Db	376	NSDDFHAIEP-DRPEFRGS--KVKEDEPTIGEDIWISPALARYIKMLASFVVSF SMLVVV	432	
Qy	513	MCLVSIIYLRAIMAVVSRSGNTLLAAWASRIASLTGSSVNLVFLILSKIYVLSLAHLVT	572	
Db	433	ISLMVTLTKIMVYNFQCTKEYTFHCWLS--AAFLPSLNTLSAMGLGAIYSNLVSRNL	490	
Qy	573	RWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNHYTLFGVRNE---	629	
Db	491	SWENHRTSEHNNSLIVKIFAFQMVNNTYSLFYVAFIRPESHGLQPN--GLFLGTEFKD	548	
Qy	630	ECAAGGCLIELAQELLVIMVGQVINNMQEVLP---KLKGWQKFLRLSKRRKAGASAG	686	
Db	549	TCLDDTCSLLALQLLTHTLIKPFPKFFKDVLVPYFVKL-----FRLRMYTSRTEARVE	602	
Qy	687	ASQGPWEDDYELVPCGLDFEYLEMVLQFGFVTIFVAACPLAPLALLNNWVEIRLDARK	746	
Db	603	I-----EDDDQ-----ANVLMFASLFLPLALLIIGFVDMRIDAHR	639	
Qy	747	FVCEYRRPVAERAQDIGIFWHLAAGLTHLAVISNAFLAFSSDFLPRAYRYWTRAHDLRG	806	
Db	640	LIWFNRKPIPIITNGIGIWLPILTFLQYCAVFTNAFIVAFSTSGFC-----	684	
Qy	807	FLNFTLARAPSSFAAHHNRTCRAFRDDDGHSYQTYNNLLAIRLAFVIVFEHVVSFVGR	866	
Db	685	-----STFLA-----DGAYC-TVQN----RLIIVIVFQNLVFLGLKY	715	
Qy	867	LLDLLVPDIPESVEIKVKREYY-----LAKQA-LAENEVLFGT	903	

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Db      716  ||  ::||  |:::  ::::  |          :||  ::||  :  :  :
Qy      904  NGTKDEQPKGSELSSHWT 921
        |  |::  |  |  |  |
Db      776  NRRKEKSNK-----KHFT 788

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RESULT 2

F96755

hypothetical protein F3N23.22 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: F96755

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Egu, P.; Feldblum, T.V.; Feng, J.; Fong, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.; Koo, H. L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Militscher, J.; Miranda, M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.; Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.; Vysotskaia, V. S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F96755

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-572 <STO>

A:Cross-references: UNIPROT:Q9SSM5; UNIPARC:UPI00000A63BD; GB:AE005173; NID:g5903091; PIDN:

AAD55649.1; GSPDB:GN00141

C:Genetics:

A:Gene: F3N23.22

A:Map position: 1

```

Query Match          5.8%; Score 288.5; DB 2; Length 572;
Best Local Similarity 20.5%; Pred. No. 3.4e-16;
Matches 169; Conservative 97; Mismatches 236; Indels 323; Gaps 29;

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Qy      142  ETFLDNLRAAGLCVDQDQDQDGNNTTVHYALLSASWAVLCYYAEDLRKLPLQELPNQASN 201
        |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      32  EVLVTELRKKGMMVDR-----VVGLAHEFLKVAAPSILGNAAAE 71

Qy      202  WSAGLLAWLGIPNVLLVEVVDVPEYYSCRFRVVKLPRFLGSDNQDFTFTSTKRHQILFE 261
        |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      72  LHIRKPTRLG-----DLPFEMQGEAFIRQPDGGLLFS-----WFERFRCYQHLIY 117

Qy      262  ILAKTPYGHEKKNLG-----IHQLLAEGVLSAFAFLHDGPFKTPPEGPQAPR 309
        :  :  ||:  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      118  GIVNSG-GHDVTLKLDGREFCWTAGESLLRRLSEGVIKQMPLHDE----- 163

Qy      310  LNQRQVLFOHWA-RWGKWN-KYQPLDHVRRYFGEKVYFAWLGFYTGWLLPAAVVGTIV 367
        :  |  |  ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      164  -LKRKELLQNWALNW-----WNCTNQPIDQIYSYFGAK----- 195

Qy      368  FLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFHDGGTVFFS 427
        |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      196  -----ELIKNLGN----- 203

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Qy      428 LFMALWAVILLEYWKRKSATLAYRWDSCSDYEDTEERPRQPQFAASAPMTAPNPITGEDEPY 487
          | | | | | | |
Db      204 -----ERAKEKEAYQRYEW----- 217

Qy      488 FPERSRARMRLAGSVVIVVMVAVVMCLVSIILYRAIMAIVVRSRGNTLLAAWASRIASL 547
          | | | | | :|:|:|:| :| :| :| :| :| :| :| :|
Db      218 FAYKRKRFRN-----DVLVIMSIIICLQLPPELAYAHIFRRIISDIIKYVLTA----- 263

Qy      548 TGSVVNLVFIILSKIYVSLAHVLTWRWEMHRTQTKFEDAFTLKVFIFQFVNFPYSSPVYIA 607
          :| :| | :|:| :| :| :| :| :| :| :| :| :| :|
Db      264 ---IYLLIIQYLTRLGGKVSVKLINREINESVEYRANSLIYKVF-----GLYFMQTYIG 314

Qy      608 FFKRGFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPLKLG 667
          | | | | | :| :| :| :| :| :| :| :| :| :| :|
Db      315 IF-----YHVLHLH-RN-----FMTLRQVLIQRLIISQVFWTLMGSLPYLKY 355

Qy      668 WWQKFRLRSKKR-KAGASAGASQ--GPWEDDY-----ELVPCGELFDEYLEMVL 713
          :|:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      356 SYRKYRARTKKMGEDSGSTGKIQIASRVEKEYFKPTYSASIGVELE---DGLFDDSLLEAL 413

Qy      714 QFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIFWHLIAGLT 773
          | | | :| | | | :| :| :| :| :| :| :| :| :| :| :|
Db      414 QFGMIMMFACAFPLAFALAAVSNVMEIRTNALKLLVTLRRPLPRAAATIGAWLNIWQFLV 473

Qy      774 HLAVISNAFFLLAFSSDFLPRAYYRWTRAHDLRGLNFTLARAPSSFAAAHNRTCRYAFR 833
          :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      474 VMSICTNSALL-----VCLY---- 488

Qy      834 DDDGHYSQTYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEI-KVK-----REY 887
          | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      489 DQEGKWK-----IEPGLAAILIMEHVLLLLKFLGSLRVPPEPAWVRASRVKNVTOAQDM 542

Qy      888 YLAKQALAENEVLFGTNGTKDEQPKGSELSSHWPTFTVPKASQLQ 932
          | | | | :| :| :| :| :| :| :| :| :| :| :|
Db      543 Y-CKQLL-----RSISGEFNSLTKEPEQQQ 567

```

RESULT 3

S48255

probable membrane protein YBR086c - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: hypothetical protein YBR0809

C;Species: *Saccharomyces cerevisiae*

C;Date: 03-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004

C;Accession: S48255; S45954; S44670

R;Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H.

Yeast 10, 1363-1381, 1994

A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.

A;Reference number: S48255; MUID:95208357; PMID:7900426

A;Accession: S48255

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-946 <MAN>

A;Cross-references: UNIPROT:P38250; UNIPARC:UPI0000036C25; EMBL:X78993; NID:g476045; PIDN:CAA55593.1; PID:g476046

R;Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994

A;Reference number: S45927

A;Accession: S45954

A;Molecule type: DNA

A;Residues: 1-946 <FE2>

A;Cross-references: UNIPARC:UPI0000036C25; EMBL:Z35955; NID:g536351; PID:g536352; MIPS:YBR086c

C;Genetics:

A;Gene: SGD:IST2
 A;Cross-references: SGD:S0000290
 A;Map position: 2R
 C;Superfamily: Saccharomyces cerevisiae probable membrane protein YBR086c
 C;Keywords: transmembrane protein
 F;131-147/Domain: transmembrane #status predicted <TM1>
 F;158-174/Domain: transmembrane #status predicted <TM2>
 F;207-243/Domain: transmembrane #status predicted <TM3>
 F;248-274/Domain: transmembrane #status predicted <TM4>
 F;302-324/Domain: transmembrane #status predicted <TM5>
 F;450-477/Domain: transmembrane #status predicted <TM6>
 F;506-532/Domain: transmembrane #status predicted <TM7>
 F;563-588/Domain: transmembrane #status predicted <TM8>

Query Match 3.7%; Score 181.5; DB 2; Length 946;
 Best Local Similarity 18.6%; Pred. No. 8.6e-07;
 Matches 118; Conservative 99; Mismatches 243; Indels 173; Gaps 25;

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Qy      342 KVALYFAWLGFPYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDPC 401
      | :|:|:| | | :|:| : | : : |
Db      119 KQSLYFAFLQNYIKWLIPFSFFGLSIRFLSNF----- 150

Qy      402 FWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRK-----SATLAYRWDCSD 456
      : : | :|:| | : | : | : |
Db      151 -----TYEFNST--YSLFAILWTLSFTAFWLYKYEPFWSDRLSKYSSFST 193

Qy      457 YEDTEERPRPQFAASAPMTAPN---PITGEDEPYFPERSRARRMLAGSVVIVMVAVVV 512
      | : : : | | : : | : : | : : |
Db      194 IEFLLQDKQKAQKASSVIMLKCCFIPVA-----LLFGA----ILLSFQL 234

Qy      513 MCLVSIIYLRAIMAIIVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVS-LAHVL 571
      | | : | : | : | : : | : : | : : |
Db      235 YCFALBIFYKQIY-----NGFMI-----SILSFLPTILICTFTPVLTVIYNKYFVEPM 282

Qy      572 TRWEMHRTQTKFEDATLKVFIQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEEC 631
      |:| | : : : | : | :|:| | :| | :| | :| | :| |
Db      283 TKWENHSSVVNAKSKAKNFVIFLSSY-VPLLLITL---FLYLPMGHLLTAERTKVF 337

Qy      632 AAGGCLIEL-----AQELLVIMVGKQVINNMQEVLIPLKGMWQK----- 671
      | | | : : : | : | : | : | : |
Db      338 NAFSILARLPHTSDSDFIIDTKRYEDQFFYFIQNLQFSMENFVSLVSIQAQKINGPN 397

Qy      672 ---FRLRSKKRKAGASAGASQGPWE--DDYELVPCEGLFD---EYLEMVLQFGFVTIFVA 723
      : | : | | : : | : | : | : : | :| : : |
Db      398 PNFWKAESIGKAQLSS-SDMKIWSKVSYQTDPNWATFDLDANFKLLQLQFGLVMFST 456

Qy      724 ACPLAPLFAALLNNVEIRLDARKFVC---EY-RRPVAERAQD-----IGIWFHILA 770
      | | | : : : :| | | | | : : : :| : |
Db      457 IWPLAPFICLIIVNLIVYQVDLRKAVLYSKPEYFFPFIYDKPSSVNTQKLTGLWNNSVLV 516

Qy      771 GLTHL-AVISNAFLAFSSDFLPRAYYRWTRAHDLRGLNFTLARAPSSFAAHHNRTCRY 829
      : | | : : | : | : : | : : |
Db      517 MFSILGCVITATLTMYQSCNIP-----GVGAHTSIHINKAWY 554

Qy      830 RAFRDDDHGHSQTYWNLLAIRLAFVIVFEHVFSVGRLLDLLVPIDIPESVEIKVKREYYL 889
      | : : : : : : | : : | : : :
Db      555 LA-----NPINHSWINI---VLYAVFIEHVSVAIFFLFSSILKSSHDDVANGIVPKHVV 605

Qy      890 AKQALAENEVL-----FGTNGTKD-EQPKGS 914
      | : | | : | : | : | | |
Db      606 NVQNPPKQEVFEKIPSPFNSNNEKELVQRKGS 638

```

RESULT 4
I48693
natural resistance-associated macrophage protein 1 - mouse
N:Alternate names: transport system membrane protein Nramp
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48693; A57071; A40739
R:Barton, C.H.; White, J.K.; Roach, T.I.; Blackwell, J.M.
J. Exp. Med. 179, 1683-1687, 1994
A:Title: NH2-terminal sequence of macrophage-expressed natural resistance-associated macrophage protein (Nramp) encodes a proline/serine-rich putative Src homology 3-binding domain.
A:Reference number: I48693; MUID:94216838; PMID:7513015
A:Accession: I48693
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-548 <RES>
A:Cross-references: UNIPROT:P41251; UNIPARC:UPI000002770F; EMBL:X75355; NID:g505155; PIDN:CAA53102.1; PID:g505156
R:Govoni, G.; Vidal, S.; Cellier, M.; Lepage, P.; Malo, D.; Gros, P.
Genomics 27, 9-19, 1995
A:Title: Genomic structure, promoter sequence, and induction of expression of the mouse Nramp1 gene in macrophages.
A:Reference number: A57071; MUID:95394476; PMID:7665187
A:Accession: A57071
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-548 <GOV>
A:Cross-references: UNIPARC:UPI000002770F
R:Vidal, S.M.; Malo, D.; Vogan, K.; Skamene, E.; Gros, P.
Cell 73, 469-485, 1993
A:Title: Natural resistance to infection with intracellular parasites: isolation of a candidate for Bcg.
A:Reference number: A40739; MUID:93258812; PMID:8490962
A:Accession: A40739
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 65-548 <VID>
A:Cross-references: UNIPARC:UPI0000178BFA
A:Note: sequence extracted from NCBI backbone (NCBIN:131666, NCBI:131667)
C:Superfamily: natural resistance-associated macrophage protein 1

Query Match 2.4%; Score 117; DB 2; Length 548;
Best Local Similarity 20.2%; Pred. No. 0.13;
Matches 136; Conservative 89; Mismatches 207; Indels 240; Gaps 34;

Qy	67	VLIDVSPPEAEKRGSYGSTAHASEPG-QQAAACRAGSPAKPRIADFLVWVEEDLKLDRQ	125
		:: :	
Db	1	MISDKSPRL-SRPSYGS-SSLPAPAPAPCR-----ETYLSEKIP	41
Qy	126	QDSAARDRTDMHRTWRET-----FLD--NLRAAGLCVDQDQVQDGNNTTVHYALLSA	174
		: : : : :	
Db	42	IPSAQDQGTSLRKLWFTGPGFLMSIAFLDPGNI-----ESDLQAGAVAGFKLLWVL	93
Qy	175	SWA---VLC-----YYAEDLRKL-----PLQELPNQ	198
		: : : :	
Db	94	LWATVLGLLCQRLAARLGVVTKDGLGEVCHLYPKVPRILLWLTIELAVGSDMQEVIGT	153
Qy	199	ASNW---SAGLLAWLGIPNVLLVVPDVPPEYSCFRVKNLPRFLGSDNQDTFTTSTKR	255
		: : : : : : :	
Db	154	AISFNLLSAGRIPLWG--GVLTITV-DTFFFLFDNYGLRKLKEAFFG-----	197
Qy	256	HQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFLPHDGPFTKTPPEGPAQPLRNQRQV	315
		: : : : : : :	

```

Db      198  --LLITIMALT-FGYE---YVVAHP--SQGALLKGLVLPTCPGCCQPELLQAVGIVGAI 249

Qy      316  LFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGLTVLVLVGCFL- 374
      :  :      | : : | || : : ||      | : | : : | : :
Db      250  MPHNIYLHSALVKSREVDRTRRVDVREANMYF-----LIEATIALSVSFIINLFVM 300

Qy      375  -VFSIDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFD-----HGG 422
      || | : : : : || : : | : : | ||      | :
Db      301  AVFGQAFYQQT--NEEAFNIC-----ANSLQNYAKIFPRDNNTVSDVIDYQGG 346

Qy      423  TVFFSLF----MALWAVLLELYWKRKSATLAY-----RWDCSDYEDTEERPRP 466
      : | | : : || | | : : | | | |      | |
Db      347  VILGCLFGPAALYWAVGLLAAGQSSMTGTGYAGQFVMEGFLKLRW----- 392

Qy      467  QFAASAPMTAPNPITGEDEPYFPERSR-ARRMLAGSVVIV--VMVAV-----V 511
      | | | : | | | : | : | : | : | :
Db      393  -----SRFARVLLTRSCAILPTVLVAVFRDLKDLGLNDL 427

Qy      512  VMCLVSIILYRAIMAVVRSRGNTLLAAWAS-RIASLTGS-----VNVLFILILSKI 563
      : | : | : | : | : | : | : | : | : | : | : | :
Db      428  LNVLSQLLLPFAVLPILTFTSMPAVMQEFANGRMKSKAITSICMALVCANLIFYVI--SY 484

Qy      564  YVSLAHVLTIRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAF----FKGRFVGYPG 618
      || | | : : | : | : : | : | : | :
Db      485  LPSLPH-----PAYFGLVALFA-IGYGLGTAYLAWTCCIAHGATFLTHSS 528

Qy      619  NYHTLFGVRNEE 630
      : | | : | | |
Db      529  HKHFLYGLPNEE 540
  
```

RESULT 5
 GNWVTC
 genome polyprotein - hepatitis C virus
 N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructural protein NS3); major envelope protein E; nonstructural protein NS1; nonstructural protein NS2; nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
 C;Species: hepatitis C virus
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C;Accession: A38465
 R;Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onishi, E.; Andoh, T.; Yoshida, I.; Okayama, H.
 J. Virol. 65, 1105-1113, 1991
 A;Title: Structure and organization of the hepatitis C virus genome isolated from human carriers.
 A;Reference number: A38465; MUID:91140698; PMID:1847440
 A;Accession: A38465
 A;Molecule type: genomic RNA
 A;Residues: 1-3010 <TAK>
 A;Cross-references: UNIPROT:P26663; UNIPARC:UPI0000131E1C; EMBL:M58335; NID:g329770; PIDN:AAA72945.1; PID:g329771
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructural protein; nucleotide binding; P-loop; polyprotein; serine proteinase; transmembrane protein
 F;2-115/Product: capsid protein C #status predicted <CPC>
 F;116-191/Product: envelope protein M #status predicted <EPM>
 F;192-389/Product: major envelope protein E #status predicted <MEE>
 F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>
 F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
 F;1007-1615/Product: hepacivirin #status predicted <NS3>
 F;1230-1237/Region: nucleotide-binding motif A (P-loop)
 F;1312-1317/Region: nucleotide-binding motif B
 F;1316-1319/Region: DEXH motif
 F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>

http://es.ScoreAccessWeb/GetItem.action?AppId=105525...24_083152_us-10-552-515-1.rpr&ItemType=4&startByte=0 (9 of 20)10/10/2008 8:49:35 AM

Db 953 LTPLRD-----WPRA----GLRDLAVAVEPVVFS 977

RESULT 6
T35404
probable squalene-hopene cyclase - *Streptomyces coelicolor*
C:Species: *Streptomyces coelicolor*
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T35404
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21577
A:Accession: T35404
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-680 <OLI>
A:Cross-references: UNIPROT:Q9X7V9; UNIPARC:UPI00000DAF47; EMBL:AL049485; PIDN:CAB39697.1; GSPDB:GN00070; SCOEDB:SC6A5.13
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC6A5.13
C:Superfamily: squalene-hopene cyclase

Query Match 2.2%; Score 110.5; DB 2; Length 680;
Best Local Similarity 22.8%; Pred. No. 0.61;
Matches 112; Conservative 52; Mismatches 173; Indels 155; Gaps 27;

```

Qy      40  MTSETSSGSHCARSMRLRRRAQEEDSTVLIDVSPPEAEKRGSGYSTAHASEPGGQAAAC 99
        ||: |: || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  MTA-TTDGSTASLRPLAASASDITDI-----PAAAGVPEAAA- 39

Qy     100  RAGSPAKPRIADFVLV-----WEEDLKLDRQQDSAADRTDMHRTWRETF-----DN 147
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      40  ----RATRATDFLLAKQDAEGWVKGDL----ETNVTMDAEDL---LLRQLGIQDEET 87

Qy     148  LRAAGLCVQDQDVQDGNNTTVHY-ALLSASWAVLCYYAEDLRLKFLQELPN---QASNW-- 202
        ||| | | : : || | | | | | | | | | | | | | | | | | | | | |
Db      88  TRAAALFIRGEQREDGTWATFYGGPGELSTTIEAYVA--LRLAGDSEAPHMARAAEWIR 145

Qy     203  SAGLLA-----WLGIPN-VLLEVVPDVPE--YYSRFRVKNLPRFLGSDNQDTFFT 251
        | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     146  SRGGIASARVFTRWLALFGWVKWDDLPELPPELIYF-----PTWVPLNIYD--FG 194

Qy     252  STKRHQI--LFEILAKTPYGHEKNLLGIHQLLAEGVLSAAFP---LHDGPFKTPPEGPQ 306
        | | | | : | | | | | | | | | | | | | | | | | | | | | |
Db     195  CWARQTIIVPLTIVSAKRP-----VRPAPFPLDELHDTDPARNPPRPL 236

Qy     307  AP-----RLNQ-----RQVLQHWARW-----GKNKYQPLDHRV 336
        || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     237  APVASWDGAFQRIDKALHAYRKVAPRLRRAAMNSAARWIIERQENDGCWGGIQP----- 291

Qy     337  RYFGEKVALYFAWLGFTYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 396
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     292  -----PAVYSVIALYLLGYDLEHPVMRAGLESLDRAVWRE-----DGARMIEA 335

Qy     397  CLDCPFW-LLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLEYWKRKSATL-----AY 450
        | | | | : ||| | | | | | | | | | | | | | | | | | | | |
Db     336  C-QSPVWDTCLATIALADAGVPEDHPQLVKASDWMMLGEQIVRPGDWSVKRPLPGGWAF 394

Qy     451  RWDCSDYEDTEE 462
        : : | | : :
Db     395  EFHNDNYPDIDD 406
    
```

RESULT 7
S46584
probable membrane protein YJL094c - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: hypothetical protein J0909
C;Species: *Saccharomyces cerevisiae*
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S46584; S56871; S47057
R;Miosga, T.; Witzel, A.; Zimmermann, F.K.
Yeast 10, 965-973, 1994
A;Title: Sequence and function analysis of a 9.46 kb fragment of *Saccharomyces cerevisiae* chromosome X.
A;Reference number: S46584; MUID:95076716; PMID:7985424
A;Accession: S46584
A;Molecule type: DNA
A;Residues: 1-873 <MIO>
A;Cross-references: UNIPROT:P40309; UNIPARC:UPI000013B5C4; EMBL:X77087; NID:g521093; PIDN:CAA54359.1; PID:g521094
A;Note: the authors translated the codon TCC for residue 645 as Trp
R;Miosga, T.; Schaaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.; Chalwatzis, N.; Fournier, C.; Schmitt, S.; Velten, C.; Wilhelm, N.; Witzel, A.; Zimmermann, F.K.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56855
A;Accession: S56871
A;Molecule type: DNA
A;Residues: 1-873 <MIW>
A;Cross-references: UNIPARC:UPI000013B5C4; EMBL:Z49369; NID:g1008267; PID:g1008268; MIPS:YJL094c
C;Genetics:
A;Gene: SGD:KHA1
A;Cross-references: SGD:S0003630
A;Map position: 10L
C;Keywords: transmembrane protein

Query Match 2.2%; Score 110.5; DB 2; Length 873;
Best Local Similarity 21.4%; Pred. No. 0.86;
Matches 69; Conservative 56; Mismatches 106; Indels 91; Gaps 16;

Qy	503	VIVVMVAVVMCLVSIIILYRAI--MAIVVSRSGNTLLAA-----W----ASRIASL	547
		: : : : : : : : : : : :	
Db	157	VFMVFIAVSISVTAFPVLCRLNELRLIKDRAGIVVLAAGIINDIMGWILLALSIIILSSA	216
Qy	548	TGSVVNVLVFILILS----KIYVSLAHVLTRWEMHRT----QTKFEDAFTLKVFIFQFVNF	599
		: : : : : : : : : : :	
Db	217	EGSPVNTVYIILLITFAWFLIYFFPLKYLRLRWVLIRTHELDKSPSLATMCILFIMFISA	276
Qy	600	YSS-----PVYIAFFKGRFVGYPGNYHTLFGVRNEEC-----AAGGLIELAQ-	642
		: : : : : : : : : :	
Db	277	YFTDIIGVHPIFGAFIAGLVVPRDDHYVVKLTERMEDIPNIVFIPYIFAVAGLNVDTLL	336
Qy	643	-----ELLVIMVGKQVINNMQEVLIPLKLG--WWQKFLRLSKRRKAGASAGASQGP	691
		: : : : : : : : : : :	
Db	337	NEGRDNGVYVFATIGIAIFTKIISG---TLTAKLTGLFWRE-----ATAAGV----	379
Qy	692	WEDDYELVPCEGLFD--EYLEMVLQFGFVT----IFVACPLAPLALLNNWVEIRLDAR	745
		: : : : : : : : : : :	
Db	380	-----LMSCKGIVEIVLTVGLNAGIISRKIFGMFV-----LMALVSTFVTPLTQL	426
Qy	746	KFVCEY---RRPVAERAQDIG	763
		: : : : :	
Db	427	VYPDSYRDGVRKSLSTPAEDDG	448

RESULT 8

T00487

Arabidopsis thaliana protein F19I3.29 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 C;Accession: T00487; B84764
 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.
 submitted to the EMBL Data Library, April 1998
 A;Description: Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence.
 A;Reference number: Z14160
 A;Accession: T00487
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-792 <ROU>
 A;Cross-references: UNIPROT:064769; UNIPARC:UPI00000485F4; EMBL:AC004238; NID:g3033373; PID:g3033401
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.J.; Gill, J. E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhagen, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: B84764
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-792 <STO>
 A;Cross-references: UNIPARC:UPI00000485F4; GB:AE002093; NID:g3033401; PIDN:AAC12845.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g35060; F19I3.29
 A;Map position: 2
 A;Introns: 50/3; 126/1; 208/1; 225/1; 312/1; 368/1; 627/2
 C;Superfamily: barley probable potassium transport protein HAK1

Query Match 2.2%; Score 110; DB 2; Length 792;
Best Local Similarity 18.5%; Pred. No. 0.83;
Matches 122; Conservative 94; Mismatches 194; Indels 250; Gaps 28;

Qy	60	AQEEEDSTVLIDVSPPEAEKRGSGYSTAHASEPGGQQAACRAGSPAKPRIADFVLVWEEED	119
		: : : : : : : : : : : : : : : : : : :	
Db	3	ARVEAATMGGEIDEEESDERGS-----	29
		: : : : : : : : : : : : : : : : : : :	
Qy	120	LKLDLRQQDSAAARDRTDMHRTWRETFL-----DNLRAAGLCV-----	155
		: : : : : : : : : : : : : : : : : : :	
Db	30	QKLDQSMDEEAGRLRNMYREKKFSALLLLQLSFQSLGVVYGLGTSPLYVFYNTFPFHGIK	89
Qy	156	DQQDVQDGNNTTVHYAL----LSASWAVLCYYAEDLRKLPLQELPNQSNWSAGLLAWLG	211
		: : : : : : : : : : : : : : : : : : :	
Db	90	DPEDIIGALSIIYSLTILPLIKKYFVVC-KAND-----NGQGQTFA---	130
Qy	212	IPNVLLEVVPDPPEEYS--CRF-RVNVKLPRFLGSDNQDFTTSTKRKHQILFEILAKTPY	268
		: : : : : : : : : : : : : : : :	
Db	131	-----LYSLLCRHAKVKTIQNQHRTDEELTYSRTTFHEHSF--AAKTKR	173
Qy	269	GHEKKN-----LLGIHQLLAEGVLSAAFP LHD--GPFKTPPEGPQAPRLNQRQVL	316
		: : : : : : : : : : : : : : : : : : :	
Db	174	WLEKRTSRKTALLILVLVGTMCVIGDGILTPAISVLSAAGGLRV----NLPHISNGVVV	228
Qy	317	F-----QHWA RWGKNKYQPLDHVRRYFGEKVALYF---AWLGFYTGWLLPAA	361
		: : : : : : : : : : : : : : : : : : :	
Db	229	FVAVVILVSLFSVOHYG-----TDRVGWLPAPIVLFWFLSIASIGMYNIWKHDTS	278

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Db 440 YSDYPD-----AYTTWNVLSSVGSIVSLASVIIIFLAILWEAFTARRL 481

RESULT 11

B86088
probable citrate permease Z5523 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B86088
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.;
Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Psofai, G.; Hackett, J.; Klink, S.; Boutin, A.; Shao,
Y.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamosis, K.; Apodaca, J.;
Anantharaman, T.S.; Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.; Blattner, F.R.
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B86088
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-438 <STO>
A;Cross-references: UNIPROT:Q8X4P7; UNIPARC:UPI00000D0D9E; GB:AE005174; NID:g12518889; PIDN:
AAG59166.1; GSPDB:GN00145; UWGP:Z5523
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z5523
C;Superfamily: citrate utilization determinant

Query Match 2.1%; Score 106; DB 2; Length 438;
Best Local Similarity 23.3%; Pred. No. 0.82;
Matches 57; Conservative 31; Mismatches 69; Indels 88; Gaps 13;

Qy	339	FGEKVAL-YFAWLGFYI-----GWLLPAADVGTGLVFLVGCFLVFS---DIP---T	381
Db	173	FGGVVALGLSAAWLPPFATGSETVMAEWGRVRF--FFIGVLLAPVGCWRLSLENDVPEPAHN	231
Qy	382	QELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDHGGTV--FFSLF-MALWAVLLL	438
Db	232	KKAAASESAFSL-----LMQHKATIAN-GILLAIGSTVATYIISLFYYGTWAAKYL	280
Qy	439	EYWKRRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFFERSRARRML	498
Db	281	-----GMNQNY-----SHAAMLL	293
Qy	499	AGSVVIVVMVAVVVMC----LVSIIYRAIMAIIVSVRSNGNTLLAAWASRIASLTGSSVNL	554
Db	294	AGVITFVGALLVGLMCDSSVGRKKLILISRMVLICSWPSEFWLLLVNPS-----PGMLLT	348
Qy	555	VFILI	559
Db	349	VFVMV	353

RESULT 12

E91240
probable membrane transport / symporter protein ECs4893 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: E91240
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Ohtsubo, E.; Nakayama, K.; Murata, T.; Tanaka, M.; Tobe, T.; Iida, T.; Takami, H.; Honda, T.; Sasakawa, C.; Ogasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001

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F:68,188,476,570/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:350,528/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #status predicted

Query Match	2.1%	Score 105;	DB 2;	Length 621;
Best Local Similarity	20.2%	Pred. No. 1.6;		
Matches	113;	Conservative 61;	Mismatches 187;	Indels 198; Gaps 29;
Qy	110	ADFLVWEE-----DLKLDROQD---SAARDRTDMHRTWRETFLDNLRA	150	
Db	102	ADLIMLVSDGDRAYFADAWSDRKGQIHLDSQDQYQLLQAQRTRDGLSLFKRPF-----	155	
Qy	151	AGLCVDQDQVQDGNNTTVH--YALLSASWAVLCYAE DLRLKLPQLPQNQASNWSAGLLA	208	
Db	156	--VTCDPKDYVIEDDTVHLVYGILEE-----PFQSL--EAINTS-----	190	
Qy	209	WLGINPVNLLEV-----VPDVPPEYISCRFRVNLPRFLGSDNQDTFF-----TS	252	
Db	191	--GLHTGLLRVQLKSEVPTSPMPEDVQTMDIRA---PDILIPDNEQTYWCYTLPFRF	245	
Qy	253	TKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAPFLHDGP--FKTPPEGQAPRL	310	
Db	246	PRHHIMYEAIV-TEGNEALVHHMEVFQCAAE---SEDFPQFNGPCDSKMKPD-----RL	296	
Qy	311	NQRQVLQHWARWGKWKYQPLD-----HVRYPGEK-----VAL	345	
Db	297	NYCRHVLAAWALGAK-AFYYPKEAGVFFGGPGSSPFLRLLEVYHNPRKIQGRQDSSGIRL	355	
Qy	346	-YFAWLGFYTGWLLPAAVVGLTVLVGCFVFSDIPTQELCGSKDSFEMCPLCLD-CPFW	403	
Db	356	PYTATLRRYDAGIMELGLVYTPLMA-----IPPQE-----TAFVLTPGCTDKCTQM	401	
Qy	404	LLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCCSDYEDTEER	463	
Db	402	ALQDSGIHFASQLHTH-----LTGRKVTVLAR-----DGQER	435	
Qy	464	PRPQFAASAPMTAPNPITGEDEPYFFPERSARRMLAGSVVIVVMVAVVMCLVSIILYRA	523	
Db	436	KE-----VNRDNHYSPPHFEIRMLKKVVTVPGDVLITSC-----	470	
Qy	524	IMAVVSRSGNTLLAAWASRIASLTGSVVNLVFLILSKIYVSLAHVLRWEMHRTQTKF	583	
Db	471	----TYNTENKTL-----ATVGG-----FGILEEMCVNYVHYYPQTELELCKSAV	511	
Qy	584	EDAFTLKVFIFQFVNFYSS 602		
Db	512	DDGFLQK--YFHMVNRFS 528		

RESULT 14

H82555
c-type cytochrome biogenesis membrane protein XF2460 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82555
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis, Sao Paulo, Brazil.
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; PMID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: H82555
A:Status: preliminary

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